

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2006, 11:28:32 ; Search time 17.6732 Seconds
(without alignments)
646.394 Million cell updates/sec

Title: US-10-680-349-42_COPY_61_86
Perfect score: 136
Sequence: 1 PINGTNSLTKKVFLKKGIDITKKDD 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	136	100.0	165	2	AAY06970 E. canis
2	136	100.0	280	5	AU96116 Ehrlichia
3	136	100.0	280	5	ABG77958 Ehrlichia
4	136	100.0	280	6	ADA09781 E. canis
5	136	100.0	280	9	ADW04274 Ehrlichia
6	97	71.3	283	2	AAY06944 E. chafee
7	97	71.3	283	5	AU96106 Ehrlichia
8	97	71.3	283	5	AU73413 Ehrlichia
9	97	71.3	283	5	ABG77936 Ehrlichia
10	97	71.3	283	6	ADA09737 E. chafee
11	97	71.3	283	9	ADW04230 Ehrlichia
12	52.5	38.6	339	8	ADN21449 Bacterial
13	52	38.2	377	6	ABU29155 Protein e
14	52	38.2	378	7	ADH88024 Enterococ
15	52	38.2	481	6	ABU20708 Protein e
16	51	37.5	525	8	ADS44601 Bacterial
17	50.5	37.1	873	8	ADS22299 Bacterial
18	50	36.8	283	9	ADW04295 Cowdria r
19	50	36.8	284	5	AU96111 Cowdria r
20	50	36.8	302	6	ABP79144 N. gonorr
21	50	36.8	302	6	ABP76775 N. gonorr
22	49.5	36.4	521	7	ABO23592 Rickettsi
23	49	36.0	235	9	ADW17535 Pinus rad
24	49	36.0	345	7	ADC00818 Enterohae

25	49	36.0	472	8	ADN46936 Thermococ
26	49	36.0	511	5	ABP65734 Bifidobac
27	49	36.0	577	5	ABP27646 Streptoco
28	49	36.0	577	6	ABU46702 Protein e
29	49	36.0	629	7	ADD68790 Streptoco
30	49	36.0	629	8	ADJ61994 Group A s
31	49	36.0	1992	2	AAW04505 Moraxella
32	49	36.0	1992	4	AAB69137 M. catarr
33	49	36.0	1992	4	AAB69133 M. catarr
34	49	36.0	2047	4	AAB69134 M. catarr
35	48.5	35.7	416	2	AAR74151 Mango cja
36	48.5	35.7	416	2	AAW44331 Class II
37	48.5	35.7	476	4	ABG99093 Pyrococcu
38	48.5	35.7	476	8	ADL23827 Pyrococcu
39	48.5	35.7	557	4	AAU20133 Human DNA
40	48.5	35.7	557	5	ABG91382 Novel hum
41	48.5	35.7	585	8	ADG32050 Mutant B
42	48.5	35.7	594	8	ADG32068 Mutant B
43	48.5	35.7	616	6	ABR41881 Predicted
44	48.5	35.7	616	6	AAE36781 Human cas
45	48.5	35.7	645	2	AAW29653 Human sec

ALIGNMENTS

RESULT 1
AAY06970 standard; protein; 165 AA.

AC AAY06970;
DT 05-JUL-1999 (first entry)

DE E. canis P30-10protein.

KW Outer membrane protein; OMP; Ehrlichia chaffeensis; E. canis; P30;
KW detection; dog.

OS Ehrlichia canis.

FN WO9913720-A1.

PD 25-MAR-1999.

PP 18-SEP-1998; 98WO-US019600.

PR 19-SEP-1997; 97US-0059353P.

PA (OHIS) UNIV OHIO STATE.

PI Rikihisa Y., Ohashi N;

DR WPI; 1999-254290/21.

PT N-PSDB; AAX34770.

PT Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia canis.

XX Disclosure; Fig 30B; 55pp; English.

CC The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chaffeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in CC AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are CC used to detect E. chaffeensis in patients and E. canis in dogs

SQ Sequence 165 AA;

Query Match 100.0%; Score 136; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 2.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

*

QY 1 PINGTNSLTKKVFGKGGDITKKDD 26
 DB 61 PINGTNSLTKKVFGKGGDITKKDD 86

RESULT 2
 AAU96116
 ID AAU96116 standard; protein; 280 AA.
 AC AAU96116;

XX 02-JUL-2002 (first entry)

XX Ehrlichia canis p28-2.

XX Ehrlichia canis infection; vaccine; serodiagnostic; p28; antibacterial.

XX Ehrlichia canis.

XX WO200222782-A2.

XX 21-MAR-2002.

XX 12-SEP-2001; 2001WO-US028759.

XX 12-SEP-2000; 2000US-00660587.

XX (RERE-) RES DEV FOUND.

XX Walker DH, Yu X, McBride JW;

XX WPI; 2002-351882/38.

XX N-PSDB; ABK68876.

XX New recombinant homologous 28 kilodalton immunodominant protein from
 PT Ehrlichia canis, useful for treating Ehrlichia canis infections.

XX Claim 16; Fig 14; 106pp; English.

XX The invention relates to a recombinant homologous 28 kDa immunodominant
 CC protein, p28, (I), of Ehrlichia canis. (I), a 28-kDa antigen preferably
 CC dispersed in a pharmaceutically acceptable carrier, is useful for
 CC inhibiting E. canis infection in a subject. (I) is useful in the
 CC development of vaccines and serodiagnostics that are particularly
 CC effective for disease prevention and serodiagnosis. AAU96100-AAU96118
 CC represent the 28-kDa antigen amino acid sequences of the invention

XX Sequence 280 AA;

Query Match 100.0%; Score 136; DB 5; Length 280;
 Best Local Similarity 100.0%; Pred. No. 4.8e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PINGTNSLTKKVFGKGGDITKKDD 26
 DB 61 PINGTNSLTKKVFGKGGDITKKDD 86

RESULT 3

ABG77958
 ID ABG77958 standard; protein; 280 AA.

XX AC ABG77958;

XX 15-NOV-2002 (first entry)

XX Ehrlichia canis outer membrane protein (P30F) #9.

XX Outer membrane protein; OMP; P30F; ehrlichiosis; infection.

XX Ehrlichia canis.

XX

PN US2002120115-A1.
 PD 29-AUG-2002.

XX 28-JAN-2002; 2002US-00059964.

XX 19-MAY-1999; 99US-00314701.

XX (RIKI/) RIKIHISA Y.

XX (OHAS/) OHASHI N.

XX Rikihisa Y, Ohashi N;

XX WPI; 2002-618954/66.

XX N-PSDB; ABS63299.

XX Isolated polynucleotide encoding an outer membrane protein of E. canis or
 PT E. chaffeensis used in the diagnosis of infection.

XX Claim 10; Fig 30B; 49pp; English.

XX The invention relates to an isolated polynucleotide encoding an outer
 CC membrane protein (OMP) of Ehrlichia canis or Ehrlichia chaffeensis used
 CC in the diagnosis of infection. An infection such as human ehrlichiosis or
 CC canine ehrlichiosis can be diagnosed by providing a serum sample from the
 CC patient, providing a polypeptide or mixture of polypeptides, contacting
 CC the sample with the polypeptide and assaying for the formation of a
 CC complex between antibodies in the serum sample and the polypeptide, where
 CC formation of a complex is indicative of infection with E. chaffeensis.
 CC This sequence represents an Ehrlichia outer membrane protein of the
 CC invention

XX Sequence 280 AA;

Query Match 100.0%; Score 136; DB 5; Length 280;
 Best Local Similarity 100.0%; Pred. No. 4.8e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PINGTNSLTKKVFGKGGDITKKDD 26
 DB 61 PINGTNSLTKKVFGKGGDITKKDD 86

RESULT 4

ADA09781

ID ADA09781 standard; protein; 280 AA.

XX AC ADA09781;

XX 06-NOV-2003 (first entry)

XX E. canis outer membrane protein p30-10.

XX outer membrane protein; circulating leukocyte; monocytic ehrlichiosis;
 XX Rocky Mountain spotted fever; canine ehrlichiosis; antigen.

XX Ehrlichia canis.

XX US6544517-B1.

XX 08-APR-2003.

XX 19-MAY-1999; 99US-00314701.

XX 18-SEP-1998; 98US-0100843P.

XX (OHIS) UNIV OHIO STATE RES. FOUND.

XX Rikihisa Y, Ohashi N;

XX WPI; 2003-553952/52.

XX N-PSDB; ADA09780.

XX

Pls mail w/ Action
2/17/06

XX Disclosure; Fig 30B; 55pp; English.

XX The invention provides isolated outer membrane proteins (OMP) from
CC Ehrlichia chaffeensis and E. canis. The E. chaffeensis proteins form part
CC of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in
CC AAY06943-958. The E. canis proteins form part of the P30 family and
CC consist of proteins shown in AAY06959-970. The proteins and genes are
CC used to detect E. chaffeensis in patients and E. canis in dogs

XX SQ Sequence 165 AA;

Query Match 48.9%; Score 715; DB 2; Length 165;
Best Local Similarity 81.9%; Pred. No. 1.8e-63;
Matches 145; Conservative 4; Mismatches 16; Indels 12; Gaps 2;

QY 1 MNYKKILVRSALISLMSILPYQSFADPVGSRNDNKGFFYISAKYNPSISHFRKFSARET 60

Db 1 MNYKKILVRSALISLMSILPYQSFADPVGSRNDNKGFFYISAKYNPSISHFRKFSARET 60

QY 61 PINGTNSLTKKVGLKKGDIITKDDFTTRVAPGIDFQNNLISGFGSGISGYMDGPRIELE 120

Db 61 PINGTNSLTKKVGLKKGDIITKDDFTTRVAPGIDFQNNLISGFGSGISGYMDGPRIELE 120

QY 121 AAYQQFNPKNPTDNDNGEYKHFALSKDAMEDDQYVVLKNDGITFMSLVNTICY 177

Db 121 AAYHNLIQKH-DNNDTNDNGEYKHF-----YLVKMPWKISHMLFLKMTAY 165

RESULT 12

AY06943
ID AAY06943 standard; protein; 281 AA.

AC AAY06943;

DT 27-AUG-2003 (revised)

DT 05-JUL-1999 (first entry)

DE E. chaffeensis OMP-1 protein.

KW Outer membrane protein; OMP; Ehrlichia chaffeensis; E. canis; P30;
KW detection; dog.

OS Ehrlichia chaffeensis.

FN WO9913720-A1.

PD 25-MAR-1999.

PF 18-SEP-1998; 98WO-US019600.

PR 19-SEP-1997; 97US-0059353P.

PA (OHIS) UNIV OHIO STATE.

PI Rikihisa Y, Ohashi N;

DR WPI; 1999-254290/21.

DR N-PSDB; AAX34743.

PT Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia
PT canis.

PS Disclosure; Fig 3B; 55pp; English.

XX The invention provides isolated outer membrane proteins (OMP) from
CC Ehrlichia chaffeensis and E. canis. The E. chaffeensis proteins form part
CC of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in
CC AAY06943-958. The E. canis proteins form part of the P30 family and
CC consist of proteins shown in AAY06959-970. The proteins and genes are
CC used to detect E. chaffeensis in patients and E. canis in dogs. (Updated
CC on 27-AUG-2003 to correct OS field.)

XX

SQ Sequence 281 AA;

Query Match 44.1%; Score 644.5; DB 2; Length 281;
Best Local Similarity 48.1%; Pred. No. 5e-56;
Matches 140; Conservative 41; Mismatches 89; Indels 21; Gaps 6;

QY 1 MNYKKILVRSALISLMSILPYQSFADPVGSRNDNKGFFYISAKYNPSISHFRKFSARET 60

Db 1 MNYKKVFTSALISLISLPGVSPDAGSGINGN---FYISGKYMPSASHFRKFSARET 56

QY 61 PINGTNSLTKKVGLKKGDIITKDDFTTRVAPGIDFQNNLISGFGSGISGYMDG 114

Db 57 ---ERNTTVGVGLKQNWDSAINSPNDVFTVSNYSFKYENPFGLGAFAGISYMDG 112

QY 115 PRIELEAAYQQFNPKNPTDNDNGEYKHFALSKDAME---DQYVVLKNDGITFMS 170

Db 113 PRIELEVSYETFDVKNGQNN--YKNEAHRYCALSHNSAADMSSANNFVFLKNEGGLDIS 170

QY 171 LMWNTCYDITAGVSVFVYACAGIGADLITTPKDLNLPAYOGKIGISYPIITPEVSAPFG 230

Db 171 FMLNACYDVWGEIGPFSPFYICAGITGLVSMFEATNPKISYQGLGLSYISPEASVFIG 230

QY 231 GYTHGVGNKKEKIPVITPVVLNDAPQ--TTSASVTLGVGEGEIGMRTP 280

Db 231 GHFKHVGNEFRDIPITITPTGSTLAGKNYPAIVLVDVCHFGIEIGRPFV 281

RESULT 13

AAU96105
ID AAU96105 standard; protein; 281 AA.

AC AAU96105;

DT 07-AUG-2003 (revised)

DT 02-JUL-2002 (first entry)

DE Ehrlichia chaffeensis P28.

KW Ehrlichia canis infection; vaccine; serodiagnostic; p28; antibacterial.

OS Ehrlichia chaffeensis.

FN WO200222782-A2.

PD 21-MAR-2002.

PF 12-SEP-2001; 2001WO-US028759.

PR 12-SEP-2000; 2000US-00660587.

PA (RERE-) RES DEV FOUND.

PI Walker DH, Yu X, McBride JW;

DR WPI; 2002-351882/38.

PT New recombinant homologous 28 kilodalton immunodominant protein from
PT Ehrlichia canis, useful for treating Ehrlichia canis infections.

PS Example 3; Fig 3; 106pp; English.

XX The invention relates to a recombinant homologous 28 kDa immunodominant
CC protein, p28, (I), of Ehrlichia canis. (I), a 28-kDa antigen preferably
CC dispersed in a pharmaceutically acceptable carrier, is useful for
CC inhibiting E. canis infection in a subject. (I) is useful in the
CC development of vaccines and serodiagnostics that are particularly
CC effective for disease prevention and serodiagnosis. AAU96100-AAU96118
CC represent the 28-kDa antigen amino acid sequences of the invention.
CC (Updated on 07-AUG-2003 to correct OS field.)

XX SQ Sequence 281 AA;

Query Match 44.1%; Score 644.5; DB 5; Length 281;

Pls. mail w/ Acton 2/17/06